



SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Beach, David H.
Demetrick, Douglas J.
Serrano, Manuel
Hannon, Gregory J.
- (ii) TITLE OF INVENTION: Cell-Cycle Regulatory Proteins, and
Uses Related Thereto
- (iii) NUMBER OF SEQUENCES: 35
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Ropes & Gray
 - (B) STREET: One International Place
 - (C) CITY: Boston
 - (D) STATE: MA
 - (E) COUNTRY: USA
 - (F) ZIP: 02110
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: WordPad
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 09/016,869
 - (B) FILING DATE: 30-JAN-1998
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/893,274
 - (B) FILING DATE: 15-JUL-1994
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/306,511
 - (B) FILING DATE: 14-SEP-1994
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/248,812
 - (B) FILING DATE: 25-MAY-1994
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/227,371
 - (B) FILING DATE: 14-APR-1994
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/154,915
 - (B) FILING DATE: 18-NOV-1993
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 07/991,997
 - (B) FILING DATE: 17-DEC-1992
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Vincent, Matthew P.
 - (B) REGISTRATION NUMBER: 36,709

(C) REFERENCE/DOCKET NUMBER: GPCI-P10-071

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: (617) 951-7739
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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 994 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 41..508

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CGGAGAGGGG GAGAACAGAC AACGGGCGGC GGGGAGCAGC ATG GAT CCG GCG GCG	55
Met Asp Pro Ala Ala	
1 5	
GGG AGC AGC ATG GAG CCT TCG GCT GAC TGG CTG GCC ACG GCC GCG GCC	103
Gly Ser Ser Met Glu Pro Ser Ala Asp Trp Leu Ala Thr Ala Ala Ala	
10 15 20	
CGG GGT CGG GTA GAG GAG GTG CGG GCG CTG CTG GAG GCG GTG GCG CTG	151
Arg Gly Arg Val Glu Glu Val Arg Ala Leu Leu Glu Ala Val Ala Leu	
25 30 35	
CCC AAC GCA CCG AAT AGT TAC GGT CGG AGG CCG ATC CAG GTC ATG ATG	199
Pro Asn Ala Pro Asn Ser Tyr Gly Arg Arg Pro Ile Gln Val Met Met	
40 45 50	
ATG GGC AGC GCC CGA GTG GCG GAG CTG CTG CTG CTC CAC GGC GCG GAG	247
Met Gly Ser Ala Arg Val Ala Glu Leu Leu Leu Leu His Gly Ala Glu	
55 60 65	
CCC AAC TGC GCC GAC CCC GCC ACT CTC ACC CGA CCC GTG CAC GAC GCT	295
Pro Asn Cys Ala Asp Pro Ala Thr Leu Thr Arg Pro Val His Asp Ala	
70 75 80 85	
GCC CGG GAG GGC TTC CTG GAC ACG CTG GTG GTG CTG CAC CGG GCC GGG	343
Ala Arg Glu Gly Phe Leu Asp Thr Leu Val Val Leu His Arg Ala Gly	
90 95 100	
GCG CGG CTG GAC GTG CGC GAT GCC TGG GGC CGT CTG CCC GTG GAC CTG	391
Ala Arg Leu Asp Val Arg Asp Ala Trp Gly Arg Leu Pro Val Asp Leu	
105 110 115	
GCT GAG GAG CTG GGC CAT CGC GAT GTC GCA CGG TAC CTG CGC GCG GCT	439
Ala Glu Glu Leu Gly His Arg Asp Val Ala Arg Tyr Leu Arg Ala Ala	
120 125 130	
GCG GGG GGC ACC AGA GGC AGT AAC CAT GCC CGC ATA GAT GCC GCG GAA	487
Ala Gly Gly Thr Arg Gly Ser Asn His Ala Arg Ile Asp Ala Ala Glu	
135 140 145	
GGT CCC TCA GAC ATC CCC GAT TGAAAGAACC AGAGAGGCTC TGAGAAACCT	538
Gly Pro Ser Asp Ile Pro Asp	
150 155	
CGGGAAACTT AGATCATCAG TCACCGAAGG TCCTACAGGG CCACAACCTGC CCCC GCCACA	598
ACCCACCCCG CTTTCGTAAGT TTTCATTTAG AAAATAGAGC TTTTAAAAAT GTCCTGCCTT	658
TTAACGTAGA TATAAGCCTT CCCCACCTAC CGTAAATGTC CATTATATATC ATTTTTTATA	718
TATTCTTATA AAAATGTAAA AAAGAAAAAC ACCGCTTCTG CTTTTTCACT GTGTTGGAGT	778
TTTCTGGAGT GAGCACTCAC GCCCTAAGCG CACATTCATG TGGGCATTTT TTGCGAGCCT	838
CGCAGCCTCC GGAAGCTGTC GACTTCATGA CAAGCATTTT GTGAAGTAGG GAAGCTCAGG	898
GGGGTTACTG GCTTCTCTTG AGTCACACTG CTAGCAAATG GCAGAACCAA AGCTCAAATA	958

AAAATAAAAT TATTTTCATT CATTCACTCA AAAAAA

994

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```

Met Asp Pro Ala Ala Gly Ser Ser Met Glu Pro Ser Ala Asp Trp Leu
 1      5      10      15
Ala Thr Ala Ala Arg Gly Arg Val Glu Glu Val Arg Ala Leu Leu
 20      25      30
Glu Ala Val Ala Leu Pro Asn Ala Pro Asn Ser Tyr Gly Arg Arg Pro
 35      40      45
Ile Gln Val Met Met Met Gly Ser Ala Arg Val Ala Glu Leu Leu Leu
 50      55      60
Leu His Gly Ala Glu Pro Asn Cys Ala Asp Pro Ala Thr Leu Thr Arg
 65      70      75      80
Pro Val His Asp Ala Ala Arg Glu Gly Phe Leu Asp Thr Leu Val Val
 85      90      95
Leu His Arg Ala Gly Ala Arg Leu Asp Val Arg Asp Ala Trp Gly Arg
100      105      110
Leu Pro Val Asp Leu Ala Glu Glu Leu Gly His Arg Asp Val Ala Arg
115      120      125
Tyr Leu Arg Ala Ala Ala Gly Gly Thr Arg Gly Ser Asn His Ala Arg
130      135      140
Ile Asp Ala Ala Glu Gly Pro Ser Asp Ile Pro Asp
145      150      155

```

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 837 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 328..738

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

```

GAGGACTCCG CGACGGTCCG CACCCTGCGG CCAGAGCGGC TTTGAGCTCG GCTGCTTCCG      60
CGCTAGGCGC TTTTTCACAG AAGCAATCCA GGCGCGCCCG CTGGTTCTTG AGCGCCAGGA      120
AAAGCCCGGA GCTAACGACC GGCCGCTCGG CACTGCACCG GGCCCCAAGC CGCAGAAGAA      180
GGACGACGGG AGGGTAATGA AGCTGAGCCC AGGTCTCCTA GGAAGGAGAG AGTGCGCCCG      240
AGCAGCGTGG GAAAGAAGGG AAGAGTGTCG TTAAGTTTAC GGCCAACGGT GGATTATCCG      300
GGCCGCTGCG CGTCTGGGGG CTGCGGA ATG CGC GAG GAG AAC AAG GGC ATG      351
                               Met Arg Glu Glu Asn Lys Gly Met
                               1      5
CCC AGT GGG GGC GGC AGC GAT GAG GGT CTG GCC ACG CCG GCG CGG GGA      399
Pro Ser Gly Gly Gly Ser Asp Glu Gly Leu Ala Thr Pro Ala Arg Gly
 10      15      20
CTA GTG GAG AAG GTG CGA CAC TCC TGG GAA GCC GGC GCG GAT CCC AAC      447

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Leu	Val	Glu	Lys	Val	Arg	His	Ser	Trp	Glu	Ala	Gly	Ala	Asp	Pro	Asn		
25					30				35						40		
GGA	GTC	AAC	CGT	TTC	GGG	AGG	CGC	GCG	ATC	CAG	GTC	ATG	ATG	ATG	GGC		495
Gly	Val	Asn	Arg	Phe	Gly	Arg	Arg	Ala	Ile	Gln	Val	Met	Met	Met	Gly		
				45				50						55			
AGC	GCC	CGC	GTG	GCG	GAG	CTG	CTG	CTG	CTC	CAC	GGC	GCG	GAG	CCC	AAC		543
Ser	Ala	Arg	Val	Ala	Glu	Leu	Leu	Leu	Leu	His	Gly	Ala	Glu	Pro	Asn		
			60					65					70				
TGC	GCA	GAC	CCT	GCC	ACT	CTC	ACC	CGA	CCG	GTG	CAT	GAT	GCT	GCC	CGG		591
Cys	Ala	Asp	Pro	Ala	Thr	Leu	Thr	Arg	Pro	Val	His	Asp	Ala	Ala	Arg		
		75					80					85					
GAG	GGC	TTC	CTG	GAC	ACG	CTG	GTG	GTG	CTG	CAC	CGG	GCC	GGG	GCG	CGG		639
Glu	Gly	Phe	Leu	Asp	Thr	Leu	Val	Val	Leu	His	Arg	Ala	Gly	Ala	Arg		
		90				95				100							
CTG	GAC	GTG	CGC	GAT	GCC	TGG	GGT	CGT	CTG	CCC	GTG	GAC	TTG	GCC	GAG		687
Leu	Asp	Val	Arg	Asp	Ala	Trp	Gly	Arg	Leu	Pro	Val	Asp	Leu	Ala	Glu		
105					110				115					120			
GAG	CGG	GGC	CAC	CGC	GAC	GTT	GCA	GGG	TAC	CTG	CGC	ACA	GCC	ACG	GGG		735
Glu	Arg	Gly	His	Arg	Asp	Val	Ala	Gly	Tyr	Leu	Arg	Thr	Ala	Thr	Gly		
				125				130					135				
GAC	TGACGCCAGG	TTCCCCAGCC	GCCCCACAACG	ACTTTATTTT	CTTACCCAAT												788
Asp																	
TTCCACCCCC	CACCCACCTA	ATTCGATGAA	GGCTGCCAAC	GGGGAGCGG													837

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Arg	Glu	Glu	Asn	Lys	Gly	Met	Pro	Ser	Gly	Gly	Gly	Ser	Asp	Glu		
1				5				10					15				
Gly	Leu	Ala	Thr	Pro	Ala	Arg	Gly	Leu	Val	Glu	Lys	Val	Arg	His	Ser		
		20					25						30				
Trp	Glu	Ala	Gly	Ala	Asp	Pro	Asn	Gly	Val	Asn	Arg	Phe	Gly	Arg	Arg		
		35					40					45					
Ala	Ile	Gln	Val	Met	Met	Met	Gly	Ser	Ala	Arg	Val	Ala	Glu	Leu	Leu		
		50				55					60						
Leu	Leu	His	Gly	Ala	Glu	Pro	Asn	Cys	Ala	Asp	Pro	Ala	Thr	Leu	Thr		
		65			70				75					80			
Arg	Pro	Val	His	Asp	Ala	Ala	Arg	Glu	Gly	Phe	Leu	Asp	Thr	Leu	Val		
			85					90						95			
Val	Leu	His	Arg	Ala	Gly	Ala	Arg	Leu	Asp	Val	Arg	Asp	Ala	Trp	Gly		
		100					105						110				
Arg	Leu	Pro	Val	Asp	Leu	Ala	Glu	Glu	Arg	Gly	His	Arg	Asp	Val	Ala		
		115				120						125					
Gly	Tyr	Leu	Arg	Thr	Ala	Thr	Gly	Asp									
	130					135											

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 853 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 213..587

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GGAGTACAGC AGCGGGAGCA TGGGTCGCAG GTTCTTGGTC ACTGTAAGGA TTCAGCGCGC	60
GGGCCGCCCA CTCCAAGAGA GGGTTTTCTT GGTGAAGTTC GTGCGATCCC GGAGACCCAG	120
GACAGCGAGC TCGCTCTGG CTTTCGTGAA CATGTTGTTG AGGCTAGAGA GGATCTTGAG	180
AAGAGGGCCG CACCGGAATC CTGGACCAGG TG ATG ATG ATG GGC AAC GTT CAC	233
Met Met Met Gly Asn Val His	
1 5	
GTA GCA GCT CTT CTG CTC AAC TAC GGT GCA GAT TCG AAC TGC GAG GAC	281
Val Ala Ala Leu Leu Leu Asn Tyr Gly Ala Asp Ser Asn Cys Glu Asp	
10 15 20	
CCC ACT ACC TTC TCC CGC CCG GTG CAC GAC GCA GCG CGG GAA GGC TTC	329
Pro Thr Thr Phe Ser Arg Pro Val His Asp Ala Ala Arg Glu Gly Phe	
25 30 35	
CTG GAC ACG CTG GTG GTG CTG CAC GGG TCA GGG GCT CGG CTG GAT GTG	377
Leu Asp Thr Leu Val Val Leu His Gly Ser Gly Ala Arg Leu Asp Val	
40 45 50 55	
CGC GAT GCC TGG GGT CGC CTG CCG CTC GAC TTG GCC CAA GAG CGG GGA	425
Arg Asp Ala Trp Gly Arg Leu Pro Leu Asp Leu Ala Gln Glu Arg Gly	
60 65 70	
CAT CAA GAC ATC GTG CGA TAT TTG CGT TCC GCT GGG TGC TCT TTG TGT	473
His Gln Asp Ile Val Arg Tyr Leu Arg Ser Ala Gly Cys Ser Leu Cys	
75 80 85	
TCC GCT GGG TGG TCT TTG TGT ACC GCT GGG AAC GTC GCC CAG ACC GAC	521
Ser Ala Gly Trp Ser Leu Cys Thr Ala Gly Asn Val Ala Gln Thr Asp	
90 95 100	
GGG CAT AGC TTC AGC TCA AGC ACG CCC AGG GCC CTG GAA CTT CGC GGC	569
Gly His Ser Phe Ser Ser Ser Thr Pro Arg Ala Leu Glu Leu Arg Gly	
105 110 115	
CAA TCC CAA GAG CAG AGC TAAATCCGCC TCAGCCCGCC TTTTCTTCT	617
Gln Ser Gln Glu Gln Ser	
120 125	
TAGCTTCACT TCTAGCGATG CTAGCGTGTC TAGCATGTGG CTTTAAAAAA TACATAATAA	677
TGCTTTTTTTT GCAATCACGG GAGGGAGCAG AGGGAGGGAG CAGAAGGAGG GAGGGAGGGA	737
GGGAGGGACC TGGACAGGAA AGGAATGGCA TGAGAAACTG AGCGAAGGCG GCCGCGAAGG	797
GAATAATGGC TGGATTGTTT AAAAAATAA AATAAAGATA CTTTTTAAAA TGTCAA	853

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

```

Met Met Met Gly Asn Val His Val Ala Ala Leu Leu Leu Asn Tyr Gly
 1             5             10             15
Ala Asp Ser Asn Cys Glu Asp Pro Thr Thr Phe Ser Arg Pro Val His
 20             25             30
Asp Ala Ala Arg Glu Gly Phe Leu Asp Thr Leu Val Val Leu His Gly
 35             40             45
Ser Gly Ala Arg Leu Asp Val Arg Asp Ala Trp Gly Arg Leu Pro Leu
 50             55             60
Asp Leu Ala Gln Glu Arg Gly His Gln Asp Ile Val Arg Tyr Leu Arg
 65             70             75             80
Ser Ala Gly Cys Ser Leu Cys Ser Ala Gly Trp Ser Leu Cys Thr Ala
 85             90             95
Gly Asn Val Ala Gln Thr Asp Gly His Ser Phe Ser Ser Ser Thr Pro
 100            105            110
Arg Ala Leu Glu Leu Arg Gly Gln Ser Gln Glu Gln Ser
 115            120            125

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(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 231 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..231

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

```

GCA CTC CTG GAA GCC GGC GCA GAT CCC AAC GCC CTG AAC CGC TTC GGG      48
Ala Leu Leu Glu Ala Gly Ala Asp Pro Asn Ala Leu Asn Arg Phe Gly
 1             5             10             15
AGG CGC CCA ATC CAG GTC ATG ATG ATG GGC AGC GCC AGG GTG GCA GAG      96
Arg Arg Pro Ile Gln Val Met Met Met Gly Ser Ala Arg Val Ala Glu
 20             25             30
CTG CTG CTG CTC CAC GGA GCA GAA CCC AAC TGC GCC GAC CCT GCC ACC      144
Leu Leu Leu Leu His Gly Ala Glu Pro Asn Cys Ala Asp Pro Ala Thr
 35             40             45
CTT ACC AGA CCT GTG CAC GAC GCA GCT CGG GAA GGC TTC CTG GAC ACG      192

```

Leu Thr Arg Pro Val His Asp Ala Ala Arg Glu Gly Phe Leu Asp Thr
 50 55 60
 CTT GTC GTG CTG CAC CGG GCA GGG GCG CGG TTG GAT GTG 231
 Leu Val Val Leu His Arg Ala Gly Ala Arg Leu Asp Val
 65 70 75

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Ala Leu Leu Glu Ala Gly Ala Asp Pro Asn Ala Leu Asn Arg Phe Gly
 1 5 10 15
 Arg Arg Pro Ile Gln Val Met Met Met Gly Ser Ala Arg Val Ala Glu
 20 25 30
 Leu Leu Leu Leu His Gly Ala Glu Pro Asn Cys Ala Asp Pro Ala Thr
 35 40 45
 Leu Thr Arg Pro Val His Asp Ala Ala Arg Glu Gly Phe Leu Asp Thr
 50 55 60
 Leu Val Val Leu His Arg Ala Gly Ala Arg Leu Asp Val
 65 70 75

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 303 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met Ala Thr Ser Arg Tyr Glu Pro Val Ala Glu Ile Gly Val Gly Ala
 1 5 10 15
 Tyr Gly Thr Val Tyr Lys Ala Xaa Asp Pro His Ser Gly His Phe Val
 20 25 30
 Ala Leu Lys Ser Val Arg Val Pro Asn Gly Gly Gly Gly Gly Gly Gly
 35 40 45
 Leu Pro Ile Ser Thr Val Arg Glu Val Ala Leu Leu Arg Arg Leu Glu
 50 55 60
 Ala Phe Glu His Pro Asn Val Val Arg Leu Met Asp Val Cys Ala Thr
 65 70 75 80

Ser	Arg	Thr	Asp	Arg	Glu	Ile	Lys	Val	Thr	Leu	Val	Phe	Glu	His	Val	85	90	95
Asp	Gln	Asp	Leu	Arg	Thr	Tyr	Leu	Asp	Lys	Ala	Pro	Pro	Pro	Gly	Leu	100	105	110
Pro	Ala	Glu	Thr	Ile	Lys	Asp	Leu	Met	Arg	Gln	Phe	Leu	Arg	Gly	Leu	115	120	125
Asp	Phe	Leu	His	Ala	Asn	Cys	Ile	Val	His	Arg	Asp	Leu	Lys	Pro	Glu	130	135	140
Asn	Ile	Leu	Val	Thr	Ser	Gly	Gly	Thr	Val	Lys	Leu	Ala	Asp	Phe	Gly	145	150	155
Leu	Ala	Arg	Ile	Tyr	Ser	Tyr	Gln	Met	Ala	Leu	Thr	Pro	Val	Val	Val	165	170	175
Thr	Leu	Trp	Tyr	Arg	Ala	Pro	Glu	Val	Leu	Leu	Gln	Ser	Thr	Tyr	Ala	180	185	190
Thr	Pro	Val	Asp	Met	Trp	Ser	Val	Gly	Cys	Ile	Phe	Ala	Glu	Met	Phe	195	200	205
Arg	Arg	Lys	Pro	Leu	Phe	Cys	Gly	Asn	Ser	Glu	Ala	Asp	Gln	Leu	Gly	210	215	220
Lys	Ile	Phe	Asp	Leu	Ile	Gly	Leu	Pro	Pro	Glu	Asp	Asp	Trp	Pro	Arg	225	230	235
Asp	Val	Ser	Leu	Pro	Arg	Gly	Ala	Phe	Pro	Pro	Arg	Gly	Pro	Arg	Pro	245	250	255
Val	Gln	Ser	Val	Val	Pro	Glu	Met	Glu	Glu	Ser	Gly	Ala	Gln	Leu	Leu	260	265	270
Leu	Glu	Met	Leu	Thr	Phe	Asn	Pro	His	Lys	Arg	Ile	Ser	Ala	Phe	Arg	275	280	285
Ala	Leu	Gln	His	Ser	Tyr	Leu	His	Lys	Asp	Glu	Gly	Asn	Pro	Glu		290	295	300

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 326 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: N-terminal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met	Glu	Lys	Asp	Gly	Leu	Cys	Arg	Ala	Asp	Gln	Gln	Tyr	Glu	Cys	Val	1	5	10	15
Ala	Glu	Ile	Gly	Glu	Gly	Ala	Tyr	Gly	Lys	Val	Phe	Lys	Ala	Xaa	Asp				

20					25					30					
Leu	Lys	Asn	Gly	Gly	Arg	Phe	Val	Ala	Leu	Lys	Arg	Val	Arg	Val	Gln
		35					40					45			
Thr	Gly	Glu	Glu	Gly	Met	Pro	Leu	Ser	Thr	Ile	Arg	Glu	Val	Ala	Val
	50					55					60				
Leu	Arg	His	Leu	Glu	Thr	Phe	Glu	His	Pro	Asn	Val	Val	Arg	Leu	Phe
65					70					75					80
Asp	Val	Cys	Thr	Val	Ser	Arg	Thr	Asp	Arg	Glu	Thr	Lys	Leu	Thr	Leu
				85					90					95	
Val	Phe	Glu	His	Val	Asp	Gln	Asp	Leu	Thr	Thr	Tyr	Leu	Asp	Lys	Val
			100					105					110		
Pro	Glu	Pro	Gly	Val	Pro	Thr	Glu	Thr	Ile	Lys	Asp	Met	Met	Phe	Gln
		115					120					125			
Leu	Leu	Arg	Gly	Leu	Asp	Phe	Leu	His	Ser	His	Arg	Val	Val	His	Arg
	130					135					140				
Asp	Leu	Lys	Pro	Gln	Asn	Ile	Leu	Val	Thr	Ser	Ser	Gly	Gln	Ile	Lys
145					150					155					160
Leu	Ala	Asp	Phe	Gly	Leu	Ala	Arg	Ile	Tyr	Ser	Phe	Gln	Met	Ala	Leu
				165				170						175	
Thr	Ser	Val	Val	Val	Thr	Leu	Trp	Tyr	Arg	Ala	Pro	Glu	Val	Leu	Leu
			180					185					190		
Gln	Ser	Ser	Tyr	Ala	Thr	Pro	Val	Asp	Leu	Trp	Ser	Val	Gly	Cys	Ile
		195					200					205			
Phe	Ala	Glu	Met	Phe	Arg	Arg	Lys	Pro	Leu	Phe	Arg	Gly	Ser	Ser	Asp
	210						215				220				
Val	Asp	Gln	Leu	Gly	Lys	Ile	Leu	Asp	Val	Ile	Gly	Leu	Pro	Gly	Glu
225					230					235					240
Glu	Asp	Trp	Pro	Arg	Asp	Val	Ala	Leu	Pro	Arg	Gln	Ala	Phe	His	Ser
				245					250					255	
Lys	Ser	Ala	Gln	Pro	Ile	Glu	Lys	Phe	Val	Thr	Asp	Ile	Asp	Glu	Leu
			260					265					270		
Gly	Lys	Asp	Leu	Leu	Leu	Lys	Cys	Leu	Thr	Phe	Asn	Pro	Ala	Lys	Arg
		275					280					285			
Ile	Ser	Ala	Tyr	Ser	Ala	Leu	Ser	His	Pro	Tyr	Phe	Gln	Asp	Leu	Glu
	290					295					300				
Arg	Cys	Lys	Glu	Asn	Leu	Asp	Ser	His	Leu	Pro	Pro	Ser	Gln	Asn	Thr
305					310					315					320
Ser	Glu	Leu	Asn	Thr	Ala										
				325											

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 85 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

```

Met Met Met Gly Xaa Xaa Xaa Val Ala Xaa Leu Leu Leu Xaa Xaa Gly
1           5           10           15
Ala Xaa Xaa Asn Cys Xaa Asp Pro Xaa Thr Xaa Xaa Xaa Arg Pro Val
          20           25           30
His Asp Ala Ala Arg Glu Gly Phe Leu Asp Thr Leu Val Val Leu His
      35           40           45
Xaa Xaa Gly Ala Arg Leu Asp Val Arg Asp Ala Trp Gly Arg Leu Pro
      50           55           60
Xaa Asp Leu Ala Xaa Glu Xaa Gly His Xaa Asp Xaa Xaa Xaa Tyr Leu
65           70           75           80
Arg Xaa Ala Xaa Gly
          85
  
```

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 157 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

```

Met Asp Pro Ala Ala Gly Ser Ser Met Glu Pro Ser Ala Asp Trp Leu
1           5           10           15
Ala Thr Ala Ala Ala Arg Gly Arg Val Glu Glu Val Arg Ala Leu Leu
          20           25           30
Glu Ala Val Ala Leu Pro Asn Ala Pro Asn Ser Tyr Gly Arg Arg Pro
      35           40           45
Ile Gln Val Met Met Met Gly Xaa Xaa Xaa Val Ala Xaa Leu Leu Leu
      50           55           60
  
```

Xaa Xaa Gly Ala Xaa Xaa Asn Cys Xaa Asp Pro Xaa Thr Xaa Xaa Xaa
65 70 75 80

Arg Pro Val His Asp Ala Ala Arg Glu Gly Phe Leu Asp Thr Leu Val
85 90 95

Val Leu His Xaa Xaa Gly Ala Arg Leu Asp Val Arg Asp Ala Trp Gly
100 105 110

Arg Leu Pro Xaa Asp Leu Ala Xaa Glu Xaa Gly His Xaa Asp Xaa Xaa
115 120 125

Xaa Tyr Leu Arg Xaa Ala Xaa Gly Gly Thr Arg Gly Ser Asn His Ala
130 135 140

Arg Ile Asp Ala Ala Glu Gly Pro Ser Asp Ile Pro Asp
145 150 155

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 138 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met Arg Glu Glu Asn Lys Gly Met Pro Ser Gly Gly Gly Ser Asp Glu
1 5 10 15

Gly Leu Ala Thr Pro Ala Arg Gly Leu Val Glu Lys Val Arg His Ser
20 25 30

Trp Glu Ala Gly Ala Asp Pro Asn Gly Val Asn Arg Phe Gly Arg Arg
35 40 45

Ala Ile Gln Val Met Met Met Gly Xaa Xaa Xaa Val Ala Xaa Leu Leu
50 55 60

Leu Xaa Xaa Gly Ala Xaa Xaa Asn Cys Xaa Asp Pro Xaa Thr Xaa Xaa
65 70 75 80

Xaa Arg Pro Val His Asp Ala Ala Arg Glu Gly Phe Leu Asp Thr Leu
85 90 95

Val Val Leu His Xaa Xaa Gly Ala Arg Leu Asp Val Arg Asp Ala Trp
100 105 110

Gly Arg Leu Pro Xaa Asp Leu Ala Xaa Glu Xaa Gly His Xaa Asp Xaa
115 120 125

Xaa Xaa Tyr Leu Arg Xaa Ala Xaa Gly Asp
130 135

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 127 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met	Met	Met	Gly	Xaa	Xaa	Xaa	Val	Ala	Xaa	Leu	Leu	Leu	Xaa	Xaa	Gly	1	5	10	15
Ala	Xaa	Xaa	Asn	Cys	Xaa	Asp	Pro	Xaa	Thr	Xaa	Xaa	Xaa	Arg	Pro	Val	20	25	30	
His	Asp	Ala	Ala	Arg	Glu	Gly	Phe	Leu	Asp	Thr	Leu	Val	Val	Leu	His	35	40	45	
Xaa	Xaa	Gly	Ala	Arg	Leu	Asp	Val	Arg	Asp	Ala	Trp	Gly	Arg	Leu	Pro	50	55	60	
Xaa	Asp	Leu	Ala	Xaa	Glu	Xaa	Gly	His	Xaa	Asp	Xaa	Xaa	Xaa	Tyr	Leu	65	70	75	80
Arg	Xaa	Ala	Xaa	Gly	Cys	Ser	Leu	Cys	Ser	Ala	Gly	Trp	Ser	Leu	Cys	85	90	95	
Thr	Ala	Gly	Asn	Val	Ala	Gln	Thr	Asp	Gly	His	Ser	Phe	Ser	Ser	Ser	100	105	110	
Thr	Pro	Arg	Ala	Leu	Glu	Leu	Arg	Gly	Gln	Ser	Gln	Glu	Gln	Ser		115	120	125	

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Val Ala Glu Ile Gly Xaa Gly Ala Tyr Gly Xaa Val Xaa Lys Ala Arg Asp
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Val Xaa Lys Ala Arg Asp
1 5

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Lys Ala Arg Asp
1

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 960 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CGGAGAGGGA ATTCGGCACGA GGCAGCATG GAGCCTTCGG CTGACTGGCT GGCCACGGCC	60
GCGGCCCCGGG GTCGGGTAGA GGAGGTGCGG GCGCTGCTGG AGGCGGTGGC GCTGCCCCAA	120
CGCACCGAAT AGTTACGGTC GGAGGCCGAT CCAGGTCATG GATGATGGGC AGCGCCCCGA	180
GTGGCGGAGC TGCTGCTGCT CCACGGCGCG GAGCCCAACT GCGCCGACCC CGCCACTCTC	240

ACCCGACCCG TGCACCACGC TGCCCGGGAG GGCTTCTGGA CACGCTGGTG GTGCTGCACC	300
GGGCCGGGGC GCGGCTGGAC GTGCGCGATG CCTGGGGCCG TCTGCCCCGTG GACCTGGCTG	360
AGGAGCTGGG CCATCGCGAT GTCGCACGGT ACCTGCGCGC CCGTGCGGGG GGCACCAGAG	420
GCAGTAACCA TGCCCGCATA GATGCCGCGG AAGGTCCCTC AGACATCCCC GATTGAAAGA	480
ACCAGAGAGG CTCTGAGAAA CCTCGGGAAA CTTAGATCAT CAGTCACCGA AGGTCCTACA	540
GGGCCACAAC TGCCCCCGCC ACAACCCACC CCGCTTTCGT AGTTTTTCATT TAGAAAATAG	600
AGCTTTTAAA AATGTCCTGC CTTTAAACGT AGATATAAGC CTTCCCCCAC TACCGTAAAT	660
GTCCATTTAT ATCATTTTTT ATATATTCTT ATAAAAATGT AAAAAAAGAA AAACACCGCT	720
TCTGCCTTTT CACTGTGTTG GAGTTTCTG GAGTGAGCAC TCACGCCCTA AGCGCACATT	780
CATGTGGGCA TTTCTTGCGA GCCTCGCAGC CTCCGGAAGC TGTCGACTTC ATGACAAGCA	840
TTTTGTGAAC TAGGGAAGCT CAGGGGGGTT ACTGGCTTCT CTTGAGTCAC ACTGCTAGCA	900
AATGGCAGAA CCAAAGCTCA AATAAAAATA AAATTATTTT CATTCAATCA CTCAAAAAA	960

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 334 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GGNGGNAAGN TGTGGGGGAA AGTTTGGGGA TGGAANACCA ANCCCTCCTT TCNTTACCAA	60
ACNCTGGCTC TGNCGAGGCT NCNTCCGANT GGTNCCCCCG GGGGAGACCC AACCTGGGNC	120
GACTTCAGGG NTGCNACATT CATTCACTAA GTGCTNGGAG NTAATANCAC CTCCTCCGAG	180
CANNGACAGG NTCGGAGGGG GCTCTTCCCC CACACCGGA GGAAGAAAGA GGAGGGNCTN	240
CGGAGAGGGG GAGAACAGAC AACGGGCGGC GGGGAGCAGC ATGGATCCGG CGGCGGGGAG	300
CAGCATGGAN CCTTCGACTG ACTGACTGCC TCGC	334

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 368 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

TCNCTTATTG	NTAGGANATA	ATAACACCTC	CACCGATAAC	TTCAC TTACA	ACGTCCCNT	60
TCCTGGAAAG	ATACACAGCG	TTCCCTCCAG	AGGATTTGTG	GGACAGGGTN	GGAGNGGTCT	120
CTTCNCCAC	CACCGGAGGA	AGAAAGAGGA	GGGGCTGNCT	G TTCACCAGA	GGGTGGGACG	180
GACCNCGTAC	GCTCGNCGNC	TNCGGAGAGG	GGGAGAGCAT	CANCGGNCGN	CGGGGAGCAA	240
CATGGAACCG	NCGGCGGGGA	GCAGCATGGA	NCCTTCGGCT	GACTGGCTGN	CCACGNCCAC	300
GNCCCGGGGT	CGGGTAGAGG	AGGTGCGGNC	GCTNCTGGAG	GCGGGGNCTC	TGNCCAACNC	360
GCTAAAAAN						368

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 404 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GACNNNCTCC	GGCCGNGTC	GGGTAGAGGA	GGTGCGGGCG	CTGCTGGAGG	CGGGGGCGCT	60
GCCCAACGCA	CCGAATAGTT	ACGGTCGGAG	GCCGATCCAG	GTNNGGGTAG	AGGGTCTGCA	120
GCGGGAGCAG	GGGATGGCGG	GCGACTCTGG	AGGACGAAGT	TTGCAGGGGA	ATTGGAATCA	180
GGTAGCGCTT	CGATTCTCCN	GAAAAAGGGG	AGGCTTCCTG	GGGAGTTTTT	AGAAGGGGTT	240
TGTAATCACA	GACCTCCTCC	TGGCGACGTC	CTGGGGGCTT	GGGAAGCCAA	GGAAGAGGAA	300
TNAGGAGCCA	CGCGGTACG	AGTCTCTCGA	ATGCTGAGAA	GATCTNAAGG	GGGGAACATA	360
TTTGTATTAG	CNTCCAAGTN	TNCTCTNTAT	CANATACAAA	NTNC		404

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 401 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CTCTNANCCC GGGTAGAGGG TCTGCAGCGG GAGCAGNGGA TGGCGGGCGA CTCTGGAGGA	60
CGAAGTTGGC AGGGGAATTG GAATCAGGTA GCGCTTCGAN TCTCCGAAA AAGGGGAGGC	120
TTCCTGGGGA GTTNNCAGAA GGGGTTTGTA ATCACAGNCC TCCNCCTGGC GACGCCCTGG	180
GGGGTTGGGA AGCCAAGGAA GAGGAATGAG GAGNCACGCG CNTACAGNTC TCTCGAATNC	240
TGANAAGATC TGAAGGGGGG AACATATTTG TATTAGNATN NAAGTATGCT CTTTATCAGA	300
TAGAAAATTC ACGAACGTGT GGNATAAAAA GGGAGTCTTA AAGAAATNTA AGATGTGCTG	360
GGACTACTTA GCCTCCAANA CACAGATNCC TGGATGGAGC T	401

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 459 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

AAAANNAAAA AAAATCTCCC AGGCCTAACA TAATTNTCAG GAAAGAAATT TCAGTAGTTG	60
NATCTCAGGG GAAATACAGG AAGTTAGCCT GGAGTAAAAG TCAGTGTGTC CCTGCCCCCTT	120
TGCTANATTG CCCGTGCCTC ACAGTGCTCT CTGCCTGTGA CGACAGCTCC NCAGAAGTTC	180
GGAGGATATA ATGGAATTCA TTGTGTACTG AAGAATGGAT AGAGAACTCA AGAAGGAAAT	240
TGGAAACTGG AAGCAAATGT AGGGGTAATT AGACACCTGG GGCTTCTGTG GGGGTCTGCT	300
TGGCGGTGAG GGGGCTCTAC ACAAGCTTCC TTTCCGTCAT GCCGNCCCCC ACCCTGGCTC	360
TGACCATTCT GTTCTCTCTG GCAGGTCATG ATGATGGGCA GCGCCCGAGG CGCGGAGCTG	420
CTGCTGCTCC ACGGCGCGGA GCCCACTGCT CCGACGCCG	459

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 390 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

AANAAAAAAG AAATNGATAA NATAGAGGAA TGAACANATT AAAATCAAAA AACANAACAN	60
AGACATAATA AAAAACGAGA ATGTTCTAGA CNTAATCATA ATTATAAAGC TCAAGACTCA	120
TTGATATNAA GGADATTGAA GGGAAATCTT AACTAGCACA ANNGNATNAA AAAANAATTC	180
CCACGACACC GCCACTCTCA ACGCATCCGT GCTCGACACT GCCCGGGAGG TCNTCCTGGA	240
CACGCTGGTG GTNCTCCACC GGNCCGGGGC ACGTCTGGAC GTGCGCGATG CCTGGGNCCG	300
NCTACCCGTG GTACCTGACT GAGGACCTGG GCCATCCCGA TTTCGCNNGG TANCTCNNGN	360
GGCTGNNGGG GCCAANAGAG GNCANTACCC	390

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 214 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

CCTGCNACGA CCCCGCCACT CTCACCCGAC CCGTGACGA CGCTGTCCGG GAGGGTTTCC	60
TGGACACGCT GGTGGTGCTG CACCGGGCCG GGGNGCGGTT GGACGTGCGC GATGCCTGGG	120
GCCGCCTNCC CGTGGNACCT GGTGAGGAG CTGGGNCATC GCGATGTCGC ACGGTACCTG	180
CGCGCGTTGC GGGGGGCACC AGAGGNNAGT NACC	214

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 235 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

NCTCTCACGG TGGGGAGGCC AACTGCGCCG AACCCGCCAC TCTACCCGA CCCGCGCACG	60
ACGGTGCCCCG GGAGGGGTTT CTGGACACGC TGGTGGTGCT GCACCGGGCC GGGGCGCGGC	120
TGGACGTTTCG NGATGCCTGG GGGNTCTNTC CGTNGNACCT GGCTGAAGAG CTGGNNCATC	180
GNGATGTCGC ACGGCCNCTG TGTGNGGNTG CGGGGGGCAC CATAGGTCAG TNTCC	235

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 573 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

NAAGTATGAG CGAAACNAAT TGTGGTTTGA GAANAGGNAA TCGTAGGGAA CTCGGGATC	60
CCNCNGGGAN CNCCAGAACC TGAGNCGCCN ATTGGAAATN ACAAACGNC TGNATCACTC	120
CGNACCAGGT NCAAAAGATA CCTGGGGANG CGGGAAGGGA AAGACNACAT CNAGACCGCC	180
TTCGCNCCTN GGNATTGTGA GCAGCCTCTG AGACTCATTN ATATNACACT CTCGTNTTTC	240
TTCTTACAAC CCTGCGGNCC GCGCGGTCGC GCTTTCTCTG CCCTCCGCCG GGTGGACCTG	300
GAGCGCTTGA GCGGTCGGCG CGCCTGGAGC AGCCAGGCGG NCAGTGGACT AGCTGCTGGA	360
CCAGGGAGGT GTGGGAGAGC GGTGGCGGCG GGTACATGCA CGTGAAGCCA TTGCGAGAAC	420
TTTATCCATA AGTATTTCAA TACCGGTAGG GACGGCAAGA GAGGAGGGCG GGATGTGCCA	480
CACATCTTTG ACCTCAGGTT TCTAACGCCT GTTTTCTTTC TGCCCTCTGC AGACAACCCC	540
CGATTGAAAG AACCAGAGAG GCTCTGAGAA ACC	573

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 434 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

CCCCATCGCG CCTTGGGANT GTGAGCNACC ATTGAGACTC ATNAATATAG CACTCGTTTT	60
TCTTCTTGCA ACCCTGCCCN CCGCGCGGTC GCGCTNTCTC TGCCCTCCGC NGGGTGGACC	120
TGGAGCGAGC GCTTGAGCGG TCGGTCGGCG CNCCTGGANC AGCCAGGCGG GCAGTGGACT	180
ACCTNCTGGA CCAGGGACCT GTGGGAGAGC GGTGNCGGCG GGTACATGCA CGTGAAGCCA	240
TTGCGAGAAC TTTATCCATA AGTATTTCAA TGCCGGTAGG GACGGCAAGA GAGGAGGGCG	300

GGATGTNCCA CACATCTTTG ACCTCAGGTT TCTAACGCCT GTTTTCTTTC TGCCCTCTGC	360
AGACATCCCC GATTGAAAGA ACCAGAGAGG CTCTGAGAAA CCTCCGGAAA CTTAGNTCAT	420
CANTCGCCGN AAAA	434

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 502 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

AGAAATTAGA TCATCAGTCA CCGATCCTCC TACAGGGNCA CAACTGNCCC CGCCACAACC	60
CACCCCGNTT TCGTAGTTTT CATTTAGAAA ATAGAGCTTT TAAAAATGTC CTGCCTTTTA	120
ACGTAGATAT ATGCCTTCCC CCACTACCGN AAATGTCCAT TTATATCATN TTTTATATAT	180
TCTTATAAAA ATGTAAAAAA GAAAAACACC GCTTCTGCCT TTTCAGTGTG TTGGAGTTTT	240
CTGGAGTGAG CACTCACGCC CTAAGCGCAC ATTCATGTGG GCATTTCTTG CGAGCCTCGC	300
AGNCTCCGGA AGCTGTCGAC CTCGAGGGGG GGNCCGGTAC CCAATTCGCC CTATAGTGAG	360
TCGTATTACA ATTCAGTGGN CGNCGNTTTT ACAACGTCGG TGGACTGGGA AAACCCCGGN	420
GTTACCCAAC TTAAATCGNC TTGGAGGACA TCCCCCTTTT CGCCAGNTGG GGTTATAGNG	480
AAGAGGGCCN CACCNNTCGC CC	502

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 503 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

CANCNATNTN CGGCATTCT NGNGAGCCTC GTAGTCTCCG GATGNTGTCTG ACCTCGAGGG	60
GGGGNCCNGT ACCCAATTCG NCCTATNGTG AGTCGTNTTA CAATTCAGTG GCCGCCGTTT	120
TNACAACGTC GNTGNACTGG GAAAACCCTG GTGTTACCCA ACTTNAATGT CCTTGNAGNA	180
CATCCCCCTT TNCGCCAGCT GGTGTAATAG CGANGAGGCC CGCACCGATC GCCCTTCCCA	240

ACAGTTGNGC AGCCTGAATG GCGAATGGAA ATTGTAAGCG TTAATATTTT GTTAAAATTC	300
GCGTTANATC NTCGGTTAAN TCAGCTCATN TTTTATCCAA TAGGCCGANA TCGGCANAAT	360
CCCCAATAAA TCAANAGAAT AGACCGAGAT AGGGTTGAGT GTCGTTCCAG TTNGGGAACA	420
NGAGTCCACT ATTAAAGANC GTAGNCTCNA ACGTCANAGG GCGAAAAACC NTNTTTCAGN	480
GGATTGGNCC ACTACGCNTA NCC	503

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 515 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

CANCNATNTN CGGCATTTCT NGNGAGCCTC GTAGTCTCCG GATGNTGTCG ACCTCGAGGG	60
GGGGNCCNGT ACCCAATTCG NCCTATNGTG AGTCGTNTTA CAATTCAGTG GCCGCCGTTT	120
TNACAACGTC GNTGNACTGG GAAAACCTG GTGTTACCCA ACTTNAATCG CCTTGNAGNA	180
CATCCCCCTT TNCGCCAGCT GGTGTAATAG CGANGAGGCC CGCACCGATC GCCCTTCCCA	240
ACAGTTGNGC AGCCTGAATG GCGAATGGAA ATTGTAAGCG TTAATATTTT GTTAAAATTC	300
GCGTTANATC NTCGGTTAAN TCAGCTCATN TTTTATCCAA TAGGCCGANA TCGGCANAAT	360
CCCCAATAAA TCAANAGAAT AGACCGAGAT AGGGTTGAGT GTCGTTCCAG TTNGGGAACA	420
NGAGTCCACT ATTAAAGANC GTAGNCTCNA ACGTCANAGG GCGAAAAACC NTNTTTCAGN	480
GGATTGGNCC ACTACGCNTA NCCATCACCC TATTC	515

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 89 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Ile Gln Val Met Met Met Gly Ser Ala Arg Val Ala Glu Leu Leu Leu Leu
 1 5 10 15
 His Gly Ala Glu Pro Asn Cys Ala Asp Pro Ala Thr Leu Thr Arg Pro Val
 20 25 30
 His Asp Ala Ala Arg Glu Gly Phe Leu Asp Thr Leu Val Val Leu His Arg
 35 40 45 50
 Ala Gly Ala Arg Leu Asp Val Arg Asp Ala Trp Gly Arg Leu Pro Val Asp
 55 60 65
 Leu Ala Glu Glu Leu Gly His Arg Asp Val Ala Arg Tyr Leu Arg Ala Ala
 70 75 80 85
 Ala Gly Gly Thr

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 88 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Ile Gln Val Met Met Met Gly Ser Ala Arg Val Ala Glu Leu Leu Leu Leu
 1 5 10 15
 His Gly Ala Glu Pro Asn Cys Ala Asp Pro Ala Thr Leu Thr Arg Pro Val
 20 25 30
 His Asp Ala Ala Arg Glu Gly Phe Leu Asp Thr Leu Val Val Leu His Arg
 35 40 45 50
 Ala Gly Ala Arg Leu Asp Val Arg Asp Ala Trp Gly Arg Leu Pro Val Asp
 55 60 65
 Leu Ala Glu Glu Arg Gly His Arg Asp Val Ala Gly Tyr Leu Arg Thr Ala
 70 75 80 85
 Thr Gly Asp

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 85 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

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Met Met Met Gly Asn Val His Val Ala Ala Leu Leu Leu Asn Tyr Gly Ala
 1           5           10           15
Asp Ser Asn Cys Glu Asp Pro Thr Thr Phe Ser Arg Pro Val His Asp Ala
      20           25           30
Ala Arg Glu Gly Phe Leu Asp Thr Leu Val Val Leu His Gly Ser Gly Ala
35           40           45           50
Arg Leu Asp Val Arg Asp Ala Trp Gly Arg Leu Pro Leu Asp Leu Ala Gln
      55           60           65
Glu Arg Gly His Gln Asp Ile Val Arg Tyr Leu Arg Ser Ala Gly Cys Ser
70           75           80           85

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(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

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Met Glu Pro Ser Ala Asp Trp Leu Ala Thr Ala Ala Ala Arg Gly Arg
 1           5           10           15
Val Glu Glu Val Arg Ala Leu Leu Glu Ala Val Ala Leu Pro Asn Ala
      20           25           30
Pro Asn Ser Tyr Gly Arg Arg Pro Ile Gln Val Met Met Met Gly Ser
      35           40           45
Ala Arg Val Ala Glu Leu Leu Leu Leu His Gly Ala Glu Pro Asn Cys
50           55           60
Ala Asp Pro Ala Thr Leu Thr Arg Pro Val His Asp Ala Ala Arg Glu
65           70           75           80
Gly Phe Leu Asp Thr Leu Val Val Leu His Arg Ala Gly Ala Arg Leu
      85           90           95
Asp Val Arg Asp Ala Trp Gly Arg Leu Pro Val Asp Leu Ala Glu Glu
      100           105           110
Leu Gly His Arg Asp Val Ala Arg Tyr Leu Arg Ala Ala Ala Gly Gly
      115           120           125
Thr Arg Gly Ser Asn His Ala Arg Ile Asp Ala Ala Glu Gly Pro Ser
130           135           140
Asp Ile Pro Asp
145

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